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Antimicrobial Peptide Protegrins Interact with DPC Micelles by Apolar Hydrophobic Cluster: Structural Studies by High-Resolution NMR Spectroscopy

Kolosova O., Usachev K., Aganov A., Klochkov V.
Kazan Federal University, 420008, Kremlevskaya 18, Kazan, Russia

Abstract

© 2016, Springer Science+Business Media New York.For the disulfide-bonded β-sheet-forming peptides which include protegrins, the presence of positively charged amino acid residues allows their strong interaction with the lipid matrix of the plasma membrane, as opposed to a protein target on the surface of the cell. We used high-resolution NMR spectroscopy for 3D structure determination of several protegrins in a solution with perdeuterated dodecylphosphocholine (DPC) micelles which is a commonly used zwitterionic detergent for the solubilization of membrane peptides and proteins. Structural studies by NMR spectroscopy of protegrins PG-1 (PDB ID: 1PG1), PG-2 (PDB ID: 2MUH), and PG-3 (PDB ID: 2MZ6) shown that the sidechains of Leu5, Phe12, Val14, and Val16 form a relatively well-ordered apolar cluster. Due to the fact that a membrane surface with positive curvature allows the hydrophobic cluster to be buried while the charged residues remain solvated in water, here we can conclude that this area could bind to the bacterial cell walls via hydrophobic and positively charged amphipathic surfaces.

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Keywords

Antibiotic, Antimicrobial peptides, NMR, Protegrin